

M. Tury

1644

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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/913,555

DATE: 12/10/98
TIME: 12:58:36

INPUT SET: S30271.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: KAYAGAKI, Nobuhiko
6 YAGITA, Kideo
7 OKUMURA, Ko
8 NAKATA, Motomi
9
10 (ii) TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFICALLY
11 REACTING WITH Fas LIGAND AND PRODUCTION PROCESS THEREOF
12
13 (iii) NUMBER OF SEQUENCES: 31
14
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: McDermott, Will & Emery
17 (B) STREET: 99 Canal Center Plaza, Suite 300
18 (C) CITY: Alexandria
19 (D) STATE: Virginia
20 (E) COUNTRY: USA
21 (F) ZIP: 22314
22
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28
29 (vi) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER: US 08/913,555
31 (B) FILING DATE: 19-SEP-1997
32 (C) CLASSIFICATION:
33
34 (viii) ATTORNEY/AGENT INFORMATION:
35 (A) NAME: Bucca Ph.D., Daniel
36 (B) REGISTRATION NUMBER: 42,368
37 (C) REFERENCE/DOCKET NUMBER: 50356-150
38
39 (ix) TELECOMMUNICATION INFORMATION:
40 (A) TELEPHONE: 202-756-8600
41 (B) TELEFAX: 202-756-8699
42
43
44 (2) INFORMATION FOR SEQ ID NO:1:
45
46 (i) SEQUENCE CHARACTERISTICS:

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47 (A) LENGTH: 120 amino acids
48 (B) TYPE: amino acid
49 (C) STRANDEDNESS: single
50 (D) TOPOLOGY: linear
51
52 (ii) MOLECULE TYPE: peptide
53
54
55
56
57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
58
59 Val Gln Leu Gln Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser
60 1 5 10 15
61
62 Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Ser Trp
63 20 25 30
64
65 Met Asn Trp Val Lys Gln Arg Pro Gly Lys Gly Leu Glu Trp Ile Gly
66 35 40 45
67
68 Arg Ile Tyr Pro Gly Asp Gly Asp Thr Asn Asp Asn Gly Lys Phe Lys
69 50 55 60
70
71 Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met
72 65 70 75 80
73
74 Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala
75 85 90 95
76
77 Arg Ser Tyr Tyr Tyr Asp Gly Ser Pro Trp Phe Thr Tyr Trp Gly Gln
78 100 105 110
79
80 Gly Thr Thr Val Thr Val Ser Ser
81 115 120
82

(2) INFORMATION FOR SEQ ID NO:2:

83
84
85 (i) SEQUENCE CHARACTERISTICS:
86 (A) LENGTH: 360 base pairs
87 (B) TYPE: nucleic acid
88 (C) STRANDEDNESS: double
89 (D) TOPOLOGY: linear
90
91 (ii) MOLECULE TYPE: cDNA to mRNA
92
93
94
95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

96 GTGCAGCTGC AGGAGTCTGG ACCTGAGCTG GTGAAGCCTG GGGCCTCAGT GAAGATTTC 60
97
98
99

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100 TGCAAGGCTT CTGGCTATGC ATTCAGTAGC TCCTGGATGA ACTGGGTGAA GCAGAGGCCT 120
101
102 GGAAAGGGTC TTGAGTGGAT TGGACGAATT TATCCTGGAG ATGGAGATAC TAACGACAAC 180
103
104 GGAAGTTCA AGGGCAAGGC CACACTGACC GCAGACAAAT CCTCCAGCAC AGCCTACATG 240
105
106 CAACTCAGCA GTCTGACATC TGAGGACTCT GCGGTCTACT TCTGTGCAAG ATCGTATTAC 300
107
108 TACGATGGTA GCCCCTGGTT TACTTACTGG GGCCAAGGGA CCACGGTCAC CGTCTCCTCA 360
109
110

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

126 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
127 1 5 10 15
128
129 Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
130 20 25 30
131
132 Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
133 35 40 45
134
135 Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
136 50 55 60
137
138 Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Pro
139 65 70 75 80
140
141 Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Ser Glu Phe Pro Trp
142 85 90 95
143
144 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
145 100 105
146

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

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153 (D) TOPOLOGY: linear

154

155 (ii) MOLECULE TYPE: cDNA to mRNA

156

157

158

159

160 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

161

162 GACATCCAGA TGACGCAGTC TCCATCCTCC CTGTCTGCCT CTCTGGGAGA CAGAGTCACC 60

163

164 ATCAGTTGCA GGGCAAGTCA GGATATTAGC AATTATTTAA ACTGGTATCA GCAGAAACCA 120

165

166 GATGGAAGTG TTAAACTCCT GATCTACTAC ACATCAAGAT TACACTCAGG AGTCCCATCA 180

167

168 AGGTTCAAGTG GCAGTGGGTC TGGGACAGAT TATTCTCTCA CCATCAGCAA CCTGGAACCT 240

169

170 GAAGATATTG CCACTTACTT TTGTCAGCAA TATAGTGAAT TTCCGTGGAC GTTCGGTGGA 300

171

172 GGCACCAAGC TGGAAATCAA ACGG 324

173

174 (2) INFORMATION FOR SEQ ID NO:5:

175

176 (i) SEQUENCE CHARACTERISTICS:

177 (A) LENGTH: 118 amino acids

178 (B) TYPE: amino acid

179 (C) STRANDEDNESS: single

180 (D) TOPOLOGY: linear

181

182 (ii) MOLECULE TYPE: peptide

183

184

185

186

187 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

188

189 Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Thr Ser
190 1 5 10 15

191

192 Val Lys Met Ser Cys Lys Ala Ala Gly Tyr Thr Phe Thr Asn Tyr Trp
193 20 25 30

194

195 Ile Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile Gly
196 35 40 45

197

198 Tyr Leu Tyr Pro Gly Gly Leu Tyr Thr Asn Tyr Asn Glu Lys Phe Lys
199 50 55 60

200

201 Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr Met
202 65 70 75 80

203

204 Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys Ala
205 85 90 95

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206
207 Arg Tyr Arg Asp Tyr Asp Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
208 100 105 110
209
210 Thr Val Thr Val Ser Ser
211 115
212

213 (2) INFORMATION FOR SEQ ID NO:6:
214

215 (i) SEQUENCE CHARACTERISTICS:
216 (A) LENGTH: 354 base pairs
217 (B) TYPE: nucleic acid
218 (C) STRANDEDNESS: double
219 (D) TOPOLOGY: linear
220

221 (ii) MOLECULE TYPE: cDNA to mRNA
222
223
224225
226 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
227

228 GTGCAGCTGC AGCAGTCAGG AGCTGAGCTG GTAAGGCCTG GGACTTCAGT GAAGATGTCC 60
229
230 TGCAAGGCTG CTGGATACAC CTTCACTAAC TACTGGATAG GTTGGGTAAA GCAGAGGCCT 120
231
232 GGACATGGCC TTGAGTGGAT TGGATATCTT TACCCTGGAG GTCTTTATAC TAACTACAAT 180
233
234 GAGAAGTTCA AGGGCAAGGC CACACTGACT GCAGACACAT CCTCCAGCAC AGCCTACATG 240
235
236 CAGCTCAGCA GCCTGACATC TGAGGACTCT GCCATCTATT ACTGTGCAAG ATACAGGGAT 300
237
238 TACGACTATG CTATGGACTA CTGGGGCCAA GGGACCACGG TCACCGTCTC CTCA 354
239

240 (2) INFORMATION FOR SEQ ID NO:7:
241

242 (i) SEQUENCE CHARACTERISTICS:
243 (A) LENGTH: 113 amino acids
244 (B) TYPE: amino acid
245 (C) STRANDEDNESS: single
246 (D) TOPOLOGY: linear
247

248 (ii) MOLECULE TYPE: peptide
249
250
251
252253 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
254

255 Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Asn Ile Gly
256 1 5 10 15
257
258 Asp Gln Ala Ser Ile S r Cys Lys Ser Thr Lys Ser Leu Leu Asn Ser

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SEQUENCE VERIFICATION REPORT
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Original Text